

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Lam, Xanthe M.
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5 Ongpipattanakul, Boonsri
Shahrokh, Zahra
Wang, Sharon X.
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Wong, Rita L.

10 (ii) TITLE OF INVENTION: Antibody Formulation

(iii) NUMBER OF SEQUENCES: 11

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Genentech, Inc.
(B) STREET: 1 DNA Way
15 (C) CITY: South San Francisco
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94080

(v) COMPUTER READABLE FORM:

20 (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: WinPatin (Genentech)

(vi) CURRENT APPLICATION DATA:

25 (A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

30 (A) APPLICATION NUMBER: 08/874897
(B) FILING DATE: 06/13/1997

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Lee, Wendy M.
(B) REGISTRATION NUMBER: 40,378
(C) REFERENCE/DOCKET NUMBER: P1089R1

35 (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 650/225-1994
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
- (B) TYPE: Amino Acid
- (C) TOPOLOGY: Linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

	Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly			
	1	5	10	15
	Gly Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Tyr Thr Phe Thr			
	20		25	30
10	Glu Tyr Thr Met His Trp Met Arg Gln Ala Pro Gly Lys Gly Leu			
	35		40	45
	Glu Trp Val Ala Gly Ile Asn Pro Lys Asn Gly Gly Thr Ser His			
	50		55	60
15	Asn Gln Arg Phe Met Asp Arg Phe Thr Ile Ser Val Asp Lys Ser			
	65		70	75
	Thr Ser Thr Ala Tyr Met Gln Met Asn Ser Leu Arg Ala Glu Asp			
	80		85	90
	Thr Ala Val Tyr Tyr Cys Ala Arg Trp Arg Gly Leu Asn Tyr Gly			
	95		100	105
20	Phe Asp Val Arg Tyr Phe Asp Val Trp Gly Gln Gly Thr Leu Val			
	110		115	120
	Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu			
	125		130	135
25	Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly			
	140		145	150
	Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp			
	155		160	165
	Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val			
	170		175	180
30	Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val			
	185		190	195
	Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn			
	200		205	210

His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys
 215 220 225

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
 230 235 240

5 Leu
 241

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 214 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
 1 5 10 15

15 Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Asn
 20 25 30

Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
 35 40 45

Leu Leu Ile Tyr Tyr Thr Ser Thr Leu His Ser Gly Val Pro Ser
 20 50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile
 65 70 75

Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
 80 85 90

25 Gly Asn Thr Leu Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu
 95 100 105

Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro
 110 115 120

30 Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
 125 130 135

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val
 140 145 150

Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu

155

160

165

Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr
 170 175 180

Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu
 5 185 190 195

Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn
 200 205 210

Arg Gly Glu Cys
 214

10 (2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Leu Gly Gly Arg Met Lys Gln Leu Glu Asp Lys Val Glu Glu Leu
 1 5 10 15

Leu Ser Lys Asn Tyr His Leu Glu Asn Glu Val Ala Arg Leu Lys
 20 25 30

20 Lys Leu Val Gly Glu Arg
 35 36

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Pro Lys Asn Ser Ser Met Ile Ser Asn Thr Pro
 1 5 10 11

30 (2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

His Gln Ser Leu Gly Thr Gln
1 5 7

5 (2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

His Gln Asn Leu Ser Asp Gly Lys
1 5 8

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 8 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

His Gln Asn Ile Ser Asp Gly Lys
20 1 5 8

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 8 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Val Ile Ser Ser His Leu Gly Gln
1 5 8

(2) INFORMATION FOR SEQ ID NO:9:

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2143 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GAATTCAACT TCTCCATACT TTGGATAAGG AAATACAGAC ATGAAAAATC 50
 TCATTGCTGA GTTGTATTAA AAGCTTTGGA GATTATCGTC ACTGCAATGC 100
 5 TTCGCAATAT GGCGCAAAAT GACCAACAGC GGTTGATTGA TCAGGTAGAG 150
 GGGCGCTGT ACGAGGTAAA GCCCGATGCC AGCATTCTG ACGACGATAC 200
 GGAGCTGCTG CGCGATTACG TAAAGAAGTT ATTGAAGCAT CCTCGTCAGT 250
 AAAAAGTTAA TCTTTCAAC AGCTGTCATA AAGTTGTCAC GGCGAGACT 300
 TATAGTCGCT TTGTTTTAT TTTTAATGT ATTGTAACT AGAATTGAG 350
 10 CTCGCCGGGG ATCCTCTAGA GGTTGAGGTG ATTATGAA AAAGAATATC 400
 GCATTTCTTC TTGCATCTAT GTTCGTTTT TCTATTGCTA CAAACGCGTA 450
 CGCTGATATC CAGATGACCC AGTCCCCGAG CTCCCTGTCC GCCTCTGTGG 500
 GCGATAGGGT CACCATCACCC TGCGTGCCA GTCAGGACAT CAACAATTAT 550
 CTGAACTGGT ATCAACAGAA ACCAGGAAAA GCTCCGAAAC TACTGATTAA 600
 15 CTATACCTCC ACCCTCCACT CTGGAGTCCC TTCTCGCTTC TCTGGTTCTG 650
 GTTCTGGGAC GGATTACACT CTGACCATCA GCAGTCTGCA ACCGGAGGAC 700
 TTGCAACTT ATTACTGTCA GCAAGGTAAT ACTCTGCCGC CGACGTTCGG 750
 ACAGGGCACG AAGGTGGAGA TCAAACGAAC TGTGGCTGCA CCATCTGTCT 800
 TCATCTTCCC GCCATCTGAT GAGCAGTTGA AATCTGGAAC TGCCTCTGTT 850
 20 GTGTGCCTGC TGAATAACTT CTATCCCAGA GAGGCCAAAG TACAGTGGAA 900
 GGTGGATAAC GCCCTCCAAT CGGGTAACTC CCAGGAGAGT GTCACAGAGC 950
 AGGACAGCAA GGACAGCACC TACAGCCTCA GCAGCACCC GACGCTGAGC 1000
 AAAGCAGACT ACGAGAAACA CAAAGTCTAC GCCTGCGAAG TCACCCATCA 1050
 GGGCCTGAGC TCGCCCGTCA CAAAGAGCTT CAACAGGGGA GAGTGTAAAG 1100

CTGATCCTCT ACGCCGGACG CATCGTGGCG CTAGTACGCA AGTTCACGTA 1150
 AAAACGGTAT CTAGAGGTTG AGGTGATTTC ATGAAAAAGA ATATCGCATT 1200
 TCTTCTTGCA TCTATGTTCG TTTTTCTAT TGCTACAAAC GCGTACGCTG 1250
 AGGTTCAAGCT GGTGGAGTCT GGCGGTGGCC TGGTGCAGCC AGGGGGCTCA 1300
 5 CTCCGTTTGT CCTGTGCAAC TTCTGGCTAC ACCTTTACCG AATACACTAT 1350
 GCACTGGATG CGTCAGGCC CGGGTAAGGG CCTGGAATGG GTTGCAGGGA 1400
 TTAATCCTAA AACCGGTGGT ACCAGCCACA ACCAGAGGTT CATGGACC GT 1450
 TTCACTATAA GCGTAGATAA ATCCACCAGT ACAGCCTACA TGCAAATGAA 1500
 CAGCCTGCGT GCTGAGGACA CTGCCGTCTA TTATTGTGCT AGATGGCGAG 1550
 10 GCCTGAAC TA CGGCTTGAC GTCCGTTATT TTGACGTCTG GGGTCAAGGA 1600
 ACCCTGGTCA CCGTCTCCTC GGCCCTCCACC AAGGGCCCAT CGGTCTTCCC 1650
 CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG GCCCTGGGCT 1700
 GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAAC TCA 1750
 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC 1800
 15 AGGACTCTAC TCCCTCAGCA GCGTGGTGAC CGTGCCTCC AGCAGCTTGG 1850
 GCACCCAGAC CTACATCTGC AACGTGAATC ACAAGCCCAG CAACACCAAG 1900
 GTCGACAAGA AAGTTGAGCC CAAATCTTGT GACAAAATC ACACATGCC 1950
 GCCGTGCCCA GCACCAGAAC TGCTGGCGG CCGCATGAAA CAGCTAGAGG 2000
 ACAAGGTCGA AGAGCTACTC TCCAAGAACT ACCACCTAGA GAATGAAGTG 2050
 20 GCAAGACTCA AAAAGCTTGT CGGGGAGCGC TAAGCATGCG ACGGCCCTAG 2100
 AGTCCCTAAC GCTCGGTTGC CGCCGGCGT TTTTTATGT TAA 2143

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 237 amino acids
 25 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

	Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe	
-23	-20	-15
		-10
	Ser Ile Ala Thr Asn Ala Tyr Ala Asp Ile Gln Met Thr Gln Ser	
5	-5	1
		5
	Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr	
	10	15
		20
	Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr Leu Asn Trp Tyr Gln	
	25	30
		35
10	Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser	
	40	45
		50
	Thr Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser	
	55	60
		65
15	Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp	
	70	75
		80
	Phe Ala Thr Tyr Tyr Cys Gln Gln Gly Asn Thr Leu Pro Pro Thr	
	85	90
		95
	Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala	
	100	105
		110
20	Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser	
	115	120
		125
	Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg	
	130	135
		140
25	Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly	
	145	150
		155
	Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr	
	160	165
		170
	Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu	
	175	180
		185
30	Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser	
	190	195
		200
	Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys	
	205	210
		214

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 300 amino acids
 (B) TYPE: Amino Acid
 5 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

	Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe			
	-23	-20	-15	-10
	Ser Ile Ala Thr Asn Ala Tyr Ala Glu Val Gln Leu Val Glu Ser			
10		-5	1	5
	Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys			
	10	15		20
	Ala Thr Ser Gly Tyr Thr Phe Thr Glu Tyr Thr Met His Trp Met			
	25	30		35
15	Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Gly Ile Asn			
	40	45		50
	Pro Lys Asn Gly Gly Thr Ser His Asn Gln Arg Phe Met Asp Arg			
	55	60		65
	Phe Thr Ile Ser Val Asp Lys Ser Thr Ser Thr Ala Tyr Met Gln			
20	70	75		80
	Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala			
	85	90		95
	Arg Trp Arg Gly Leu Asn Tyr Gly Phe Asp Val Arg Tyr Phe Asp			
	100	105		110
25	Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr			
	115	120		125
	Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr			
	130	135		140
30	Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe			
	145	150		155
	Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser			
	160	165		170
	Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr			

175

180

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Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr
190 195 200

Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys
5 205 210 215

Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
220 225 230

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Arg Met Lys
235 240 245

10 Gln Leu Glu Asp Lys Val Glu Glu Leu Leu Ser Lys Asn Tyr His
250 255 260

Leu Glu Asn Glu Val Ala Arg Leu Lys Lys Leu Val Gly Glu Arg
265 270 275 277